

Db 1346 actgaccaggaggacatcatcaaaaggaatatccagagtgatcagcagagggagctcca 1405
 Qy 1026 gatctctctgctatcagtcaccacacaaactaactggtggtcttaaaagctcg 1085
 Db 1406 ggtgctctgctatcagtcaccacacaaactaactggtggtcttaaaagctcg 1465
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 Db 1466 acactgcaagaatggatgctcggctctcagtgtaactcttatgtcaagggtgaacct 1525
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 Db 1526 ctactacggcagaagcattgccaagaagaacacccatgtgaagaagtgcactttgaa 1585
 Qy 1203 tgcagtgctcaatgagctgttctgttatcttctgtgagggccttgagataaag 1262
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 Qy 1323 agtcttggtgtca---gcagcagaaggaaactggtgagagcactggaaagagatctgtga 1379
 Db 1706 gatcctgggggcacacagtgctcacagcagtggtgctgaaacactggagagaggtctgca 1765
 Qy 1380 ctacccaggagacaaattgcgaatggcagctgctctgtga 1421
 Db 1766 gagccccgaagctgtggcgaagtggcagactgctgagcga 1807

RESULT 7
 AAX41151
 ID AAX41151 standard; cDNA; 424 BP.
 XX
 AC AAX41151;
 XX
 DT 17-JUN-1999 (first entry)
 XX
 DE Human secreted protein 5' EST SEQ ID NO:95.
 XX
 KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
 KW forensic; gene therapy; chromosome mapping; signal peptide;
 KW upstream regulatory sequence; cytokine activity; cell proliferation;
 KW differentiation; haematopoiesis regulation; tissue growth regulation;
 KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0906548-A2.
 XX
 PD 11-FEB-1999.
 XX
 PF 31-JUL-1998; 98WO-1801222.
 XX
 PR 01-AUG-1997; 97US-0905135.
 XX
 PA (GEST) GENSET.
 XX
 PI Duclert A, Dumas Milne Edwards J, Lacroix B;
 XX
 DR WPI; 1999-153778/13.
 DR P-PSDB; AAY12318.
 XX
 PT New nucleic acids encoding human secreted proteins - obtained from
 PT cDNA libraries prepared from e.g. liver, ovary, brain, prostate,
 PT kidney, lung, umbilical cord, placenta and colon tissue
 XX
 PS Claim 1; Page 243; 824pp; English.
 XX
 CC AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AAY12261 to

CC AAY12514, respectively. The proteins given represent the signal peptide
 CC and an N-terminal fragment of a secreted protein. The nucleic acid
 CC sequences can be used for producing secreted human gene products. They
 CC can also be used to develop products for diagnosis and therapy. The
 CC proteins obtained may have cytokine activity, cell
 CC proliferation/differentiation activity, haematopoiesis regulating
 CC activity, tissue growth regulating activity, reproductive hormone
 CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
 CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
 CC activity, tumour inhibition activity or other activities. The products
 CC can be used in forensic, gene therapy and chromosome mapping procedures.
 CC The sequences can also be used for obtaining corresponding promoter
 CC sequences. The nucleic acids encoding the signal peptide can be used for
 CC directing extracellular secretion of a polypeptide or the insertion of a
 CC polypeptide into a membrane, or importing a polypeptide into a cell.
 XX
 SQ Sequence 424 BP; 109 A; 112 C; 104 G; 98 T; 1 other;
 Query Match 9.3%; Score 361; DB 20; Length 424;
 Best Local Similarity 99.4%; Pred. No. 4.4e-72;
 Matches 361; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ctcttgcctccctccctgttccagagagctggtgctggtggtggtggtggttcttcag 60
 Db 62 ctcttgcctccctccctgttccagagagctggtgctggtggtggtggttcttcag 121
 QY 61 cgttcgaaagccggtgctgagatccagcaggaagtgaatccagcagcagcagcagcagc 120
 Db 122 cgttcgaaagccggtgctgagatccagcaggaagtgaatccagcagcagcagcagcagc 181
 QY 121 cagcactcggacagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
 Db 182 cagcactcggacagacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 241
 QY 181 ttgatgaaatcccccagctggtggtggtggtggtggtggtggtggtggtggtggtggtg 240
 Db 242 ttgatgaaatcccccagctggtggtggtggtggtggtggtggtggtggtggtggtggtg 301
 QY 241 tctcttgcagtgatctgctgctgctgctgctgctgctgctgctgctgctgctgctgctcca 300
 Db 302 tctcttgcagtgatctgctgctgctgctgctgctgctgctgctgctgctgctgctgctcca 361
 QY 301 tacaagtttgcagtgatctgctgctgctgctgctgctgctgctgctgctgctgctgctgctcca 360
 Db 362 tacaagtttgcagtgatctgctgctgctgctgctgctgctgctgctgctgctgctgctgctcca 421
 QY 361 aag 363
 Db 422 aag 424

RESULT 8
 AAT25277
 ID AAT25277 standard; cDNA to mRNA; 318 BP.
 XX
 AC AAT25277;
 XX
 DT 25-NOV-1996 (first entry)
 XX
 DE Human gene signature HUMGS07439.
 XX
 KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 KW human; cloning; mapping; non-biased library; diagnosis; detection;
 KW cell typing; abnormal cell function; ss.
 OS Homo sapiens.
 XX
 PN W09514772-Al.
 XX
 PD 01-JUN-1995.
 XX
 PF 11-NOV-1994; 94WO-JP01916.

XX 12-NOV-1993; 93JP-0355504.
 XX (MATS/) MATSUBARA K.
 PA (OKUBO/) OKUBO K.
 XX Matsubara K, Okubo K;
 XX WPI; 1995-206931/27.
 DR
 XX
 XX Identifying gene signatures in 3'-directed human cDNA library - e.g.
 PT for diagnosis of abnormal cell function, by preparing cDNA that
 PT reflects relative abundance of corresp. mRNA in specific human
 PT tissues
 XX
 XX Claim 1; Page 1811; 2245pp; Japanese.
 PS
 XX A single-stranded DNA (or its complementary strand or the corresp.
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
 CC given in AAT19001-T26837 and which is able to hybridise to part of
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
 CC sequences were obtained from 3'-directed cDNA libraries prepared
 CC from various human tissues; synthesis of cDNA was initiated from the
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
 CC all the 3'-oriented cDNAs hybridise with specific mRNA species, almost
 CC is constructed so as to reflect accurately the relative abundance of
 CC different mRNAs in the particular tissue from which it was derived.
 CC The appearance frequency of a given GS in a cDNA library can be
 CC determined (esp. using primers and probes derived from the GS
 CC sequences) as a means of diagnosing abnormal cell function or for
 CC recognising different cell types.
 XX
 XX Sequence 318 BP; 80 A; 48 C; 66 G; 115 T; 9 other;
 SQ
 Query Match 6.8%; Score 264.2; DB 16; Length 318;
 Best Local Similarity 94.2%; Pred. NO. 2.7e-50;
 Matches 291; Conservative 0; Mismatches 16; Indels 2; Gaps 2;
 QY 3535 gatcttaataccttaatttcattctgtcgaataatgtactgttttagaattattacaat 3594
 Db 1 gatcttaataccttaatttcattctgtcgaataatgtactgttttagaattattacaat 59
 QY 3595 atcaatgtgaatatattgtgaattctgttacaatactgcactgtattacaatgtataatta 3654
 Db 60 atcaatgtgaatatattgtgaattctgttacaatactgcactgtattacaatgtataatta 119
 QY 3555 attgtgtctgtattagccaattctcaccaccacccaatggggagggtatacatgtttgaagaa 3714
 Db 20 attgtgtctgtattagccaattctcaccaccacccaatggggagggtatacatgtttgaagaa 179
 QY 3715 c-gtgaactcggtaattgattgttctgtattgttgaactcaatagagtggtttggaag 3773
 Db 180 ctgtgaactcagtaattgattgttctgtattgttgaactcaatagagtggtttggaag 239
 QY 3774 gaagcatggtgtgagacagtgctgtctcttttggccagctctgtatgtttgttaa 3833
 Db 240 gnaagcatggtgtgagcagtgctgtctcttttggccagctctgtatgtttgttaa 299
 QY 3834 gaccatgtt 3842
 Db 300 gccntgttt 308
 RESULT 9
 AAI10603/C
 ID AAI10603 standard; DNA; 383 BP.
 XX
 AC AAI10603;
 XX
 DT 12-OCT-2001 (first entry)
 XX

DE Probe #536 for gene expression analysis in human cervical cell sample.
 XX
 KW Probe: human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer; ss.
 XX
 OS Homo sapiens.
 XX WO200157278-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US00670.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0632366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488901/53.
 XX
 XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human cervical epithelial cells -
 PT
 PS Claim 25; SEQ ID NO 536; 487pp; English.
 XX

CC The present invention relates to human single exon nucleic acid probes
 CC (SENPs). The present sequence is one such probe. The SENPs are derived
 CC from human HeLa cells. The SENPs can be used to produce a single exon
 CC microarray, which can be used for measuring human gene expression in a
 CC sample derived from human cervical epithelial cells. By measuring gene
 CC expression, the probes are therefore useful in grading and/or staging
 CC of diseases of the cervix, notably cervical cancer.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX

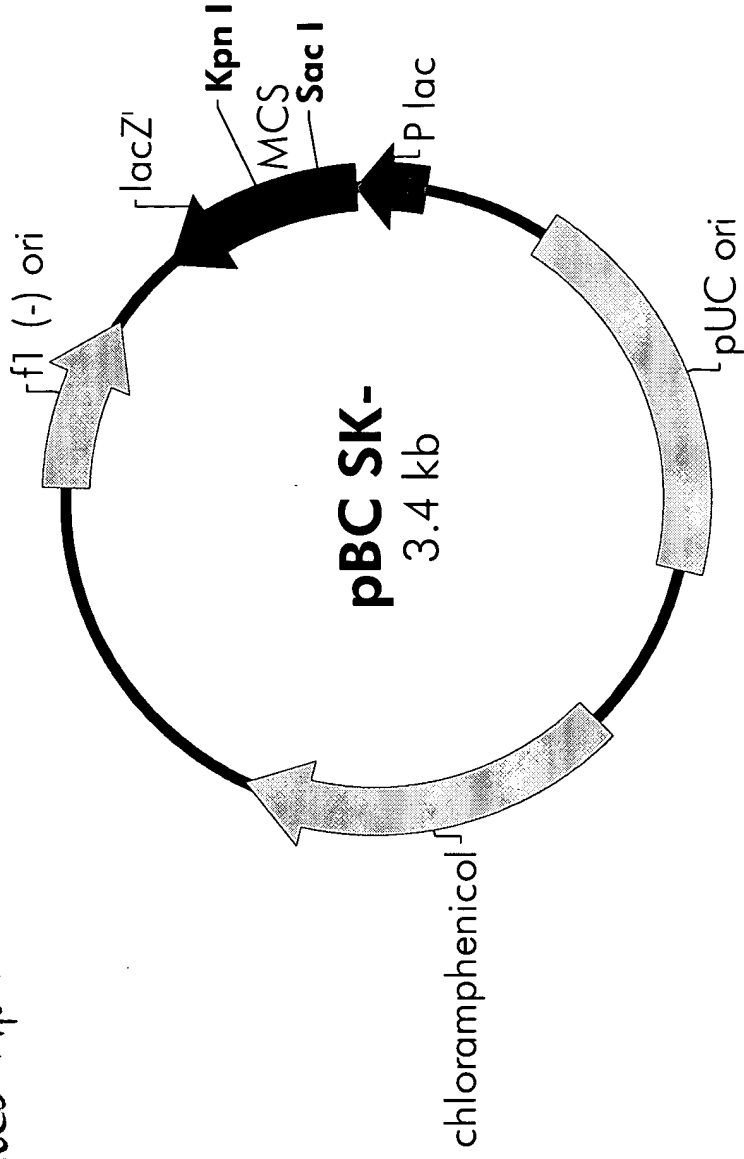
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Query Match 5.6%; Score 216.6; DB 22; Length 383;
 Best Local Similarity 95.8%; Pred. NO. 1.6e-39;
 Matches 254; Conservative 0; Mismatches 6; Indels 5; Gaps 3;
 QY 737 tgacgatctctccagagaagcataaagtgaatactagagtgtctgagaaaaaccttg 796
 Db 383 TGACGATCTCTCCAGAGAAGCATAAAGTGAAGTGAAGTGTCTGAGAAAAACCTTGG 324
 QY 797 atccagcttttgatgagacatttacattctatgggtaccctacaccccaatcc---aag 853
 Db 323 ATCCAGCTTTTGATGAGACCTTTTACATTCTATGGGATACCTACACCCAAATCCNNAAGA 264
 QY 854 aattggccttgcaactcacaat-tttgagttttgacaggttttcaaga-gatgatatcat 911
 Db 263 ATTGGNCCCTTGACATTCACAATNTTTGAGGTTTTCAGAGNGATGATATCAT 204
 QY 912 tgggggaagttctaattcctctctcgcggaattgaattatctgaagaaaaattttaaataa 971
 Db 203 TGGGGAAGTTCTAATTCCTCTCTCGGGAATTGAATATCTGAGGAAAAAATGTTAATGAA 144
 QY 972 tagagagatcatcaagagaaatggtt 996
 Db 143 TAGAGAGATCATCAAGAGAAATGNT 119

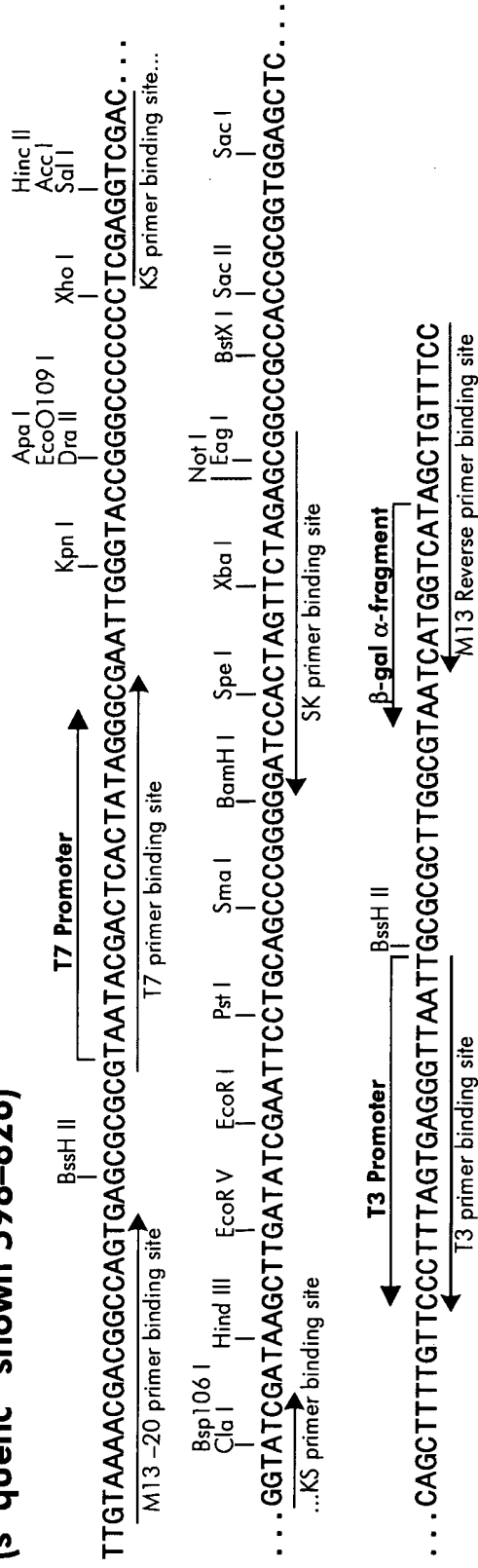
RESULT 10
 AAI1857/C

p Bluescript+

f1 (-) origin 21-327
 β-galactosidase α-fragment 460-816
 multiple cloning site 653-760
 lac promoter 817-938
 pUC origin 1158-1825
 chloramphenicol resistance ORF 1976-2833



pBC SK (+/-) Multiple Cloning Site Region (sequence shown 598-826)



Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1981 Std Error: 0.00
 Seq primer: -400P from Gibco
 High quality sequence stop: 444.
 Location/Qualifiers
 1. 499
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1947675"
 /clone_lib="NCI-CGAP GC4"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; 1st strand cDNA was prepared from 3 pooled
 germ cell tumors, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT7n3
 vector. Library is normalized. Library was constructed by
 Bento Soares and M. Fatima Bonaldo."
 BASE COUNT 171 a 95 c 60 g 173 t
 ORIGIN

Query Match 12.2%; Score 474.4; DB 10; Length 499;
 Best Local Similarity 99.4%; Pred. No. 3.6e-83;
 Matches 497; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
 QY 3389 tttaaatataaaggataattgttaaatgttttttagcttttaaaatttaaagtgtttt 3448
 Db 499 TTTAAATATAAATGGATAATTTGTAATAGTTTAACTTTTAAATTTAAAGTGT 440
 QY 3449 tgagtgtgaaagtgtgtaaaactatttgcacactgttttcgaaagagaagaagaaac 3508
 Db 439 TGAGTGTGAAAGTGTGTAAGTAACTATTTCGAACCTGTTTCAGAAAGAGAAAGAAC 380
 QY 3509 acaaaaggaattgaaacaggcaggagagactttaataacttaatttcatttcgtgcaaaa 3568
 Db 379 AACAAAGGAATGAAACAGCGGAGAGACTTAATACCTTAATTCATCATTTCTG-AAAA 321
 QY 3569 tgtactgttttagaagtattacaaatcaatgtgaatatcttgaaatcctgtgtacaaatc 3628
 320 TGTACTGTTTGAAGTGTATTACAATATCAATGTGATATCTTGAACTCTGTACAAATC 261
 QY 3629 ctgcaactgtataaactgataaattgtttgtctgattagccaatctcacaccacaa 3688
 Db 260 CTGCACGTGATTAAACATGTAAATTAATTTGTTCTGTGATTAGCAATCTCACACCACAA 201
 QY 3689 atggggagggtatcatatttgaagaac-gtgaactcggtaattgattgtctgtatgtt 3747
 Db 200 ATGGGAGGGTATACATGTTTCAGAACTGTGTAACTCAGTAATTTGTTCTGTATGT 141
 QY 3748 gtaactcaatagaagtgttttggagaagaactgtgtgtgtgagacagtctgtttttt 3807
 Db 140 GTRACTCAATGAAGTCTTTTGGNAGGAGCAGTGGTGTGTGAGACAGTGTCTGTTCTTT 81
 QY 3808 gtgccagctctgtatgtttgtgaagaccattgtttgtaagacatgaataaaattgtct 3867
 Db 80 GTGCCAGCTCTGTATGATGTTTGTGAAGACCATGTTTGTAGACATGAAATAAATTGCTGCT 21
 QY 3868 ttgtcccaaaaaaataaaaa 3887
 Db 20 TTTGCCCAAAAAAATAAAAA 1

RESULT 12
 AA081755

LOCUS AA081755 518 bp mRNA EST 21-OCT-1996
 DEFINITION zn22d07.r1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens
 CDNA clone IMAGE:548173 5' similar to SW:SYT4_MOUSE P40749
 SYNAPTOFAGMIN IV. ; mRNA sequence.
 ACCESSION AA081755
 VERSION AA081755.1 GI:1623814
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 518)
 AUTHORS Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
 Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins,
 M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
 B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
 Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,
 Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Warra, M.,
 Generation and analysis of 280,000 human expressed sequence tags
 Genome Res. 6 (9), 807-828 (1996)
 97044478
 COMMENT Contact: Wilton RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 309.
 FEATURES
 Location/Qualifiers
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 /dev_stage="Ntera-2/RA+MI neuroepithelial cells"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Vector: pBluescript SK-; Site:1: EcoRI; Site:2:
 XhoI; Cloned unidirectionally. Primer: Oligo dT. NT2
 (Ntera-2/ci.D1) precursor cells induced with Retinoic
 Acid for 1 week, followed by 3 weeks in mitotic inhibitors
 (Replate #2). Average insert size: 1.1 kb; Uni-ZAP XR
 Vector; -5' adaptor sequence: 5' GAATTCGGCAGGAG 3' -3'
 adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'
 BASE COUNT 160 a 118 c 112 g 126 t 2 others
 ORIGIN
 Query Match 11.9%; Score 453.8; DB 10; Length 518;
 Best Local Similarity 98.5%; Pred. No. 4.3e-81;
 Matches 509; Conservative 0; Mismatches 4; Indels 4; Gaps 4;
 QY 68 aaagccgcycttggatccagcgaagtgaatccagcaggcaggtttcccttcagcaac 127
 Db 1 AAAGCGGCGCTTGAGATCCAGCAAGTGAATCCAGCCAGGCGAGTTTCCCTTCAGCAC 60
 QY 128 tcggacagaacacgcagtaaaaaatggctccgcatcacaccacgcgggaagattgatg 187
 Db 61 TCGGACAGAACACGCAGTAAATAATGGTCCGATCACACACGCCGGGAAGAAATTGATG 120
 QY 188 aaatccccacagtggtggggatcttcagtgcaatttggcctgtgttcacagctctctct 247
 Db 121 AAATCCCAACAGTGTG-TGGATCTTCAGTGCATTTGGCTGTCTTCACAGTCTCTCT 179
 QY 248 ttgcattgatctgtgtcagagaaatcatccaagtcttaacaaagactcctccatacaagt 307
 Db 180 TTGCATGATGCTGTGTGAGAGAAATCATCCAGTCTTAACAAGACTCTCTCCATCAAGT 239
 QY 308 ttgtcattgtcttaaggagggttgattattaccctgaaacctaataaagcaaaagaagt 367
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Db 240 TTGTGATGCTTAAAGGAGTTGATATTACCTGAAACCTAAATAGCAAAAAGAGT 299
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Qy 428 atctgagcttgaaagaagagagatctcaatgccaattttcccaaaaaccacacacac 487
Db 359 ATCTGATCTTTGAAAGAGAGATCTCAATGTCGAATTTTCCCAAAACCAACNTCAAACCTG 418
Qy 488 ggaagctctctgagctgagagatgcaaccgagagctctttttgagaaggggaaagaagt 547
Db 419 GCAGTCTTCTGATCTGGAGATGCAACCCGAGACTCTTTTGAAGGGGGAAGAAGT 478
Qy 548 cagtttccctcagagagtttaagtcagacactccct 584
Db 479 CAGTTT-CCCTGAGAGTTT-AGTCCGACACTNCT 513

RESULT 13
AV606332 565 bp mRNA EST 30-AUG-2000
DEFINITION AV606332 Bos taurus kidney fetus Bos taurus cDNA clone EIKI034B06
5', mRNA sequence.
ACCESSION AV606332
VERSION AV606332.1 GI:9736705
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 565)
AUTHORS Sugimoto,Y., Hirotsune,S., Takasuga,A., Itoh,R., Jitohzono,A. and
Suzuki,H.
TITLE bovine cDNA sequencing
COMMENT Unpublished (2000)
Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@ccoc.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
FEATURES
Source
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/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="EIKI034B06"
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BASE COUNT 162 a 110 c 144 g 148 t 1 others
ORIGIN
Query Match 11.8%; Score 458; DB 10; Length 565;
Best Local Similarity 90.3%; Pred. No. 5.9e-80;
Matches 501; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

Qy 915 ggaagttcattctctcgcgaattgaattatctgaaggaataatgttaataagatag 974
Db 11 GGAAGTCTGATTCCTCGGAGGAATGAATTAACATAAGGGAATGTAAATGAACAG 70
Qy 975 agagatcatcaagaagaatgttagaagcttccagagcggggtgagttactgactctct 1034
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Qy 1035 ctgctatcagtcaccacacaaacactctaaactgtggtgtcttaaaagctcgacatctgcc 1094
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Qy 1095 taaatctgagtgtccgggaacttccagatccctatgtcaaaagtgaacctgtaccatgccaa 1154
Db 191 TAAATCTGATGTCTGTGGACTTTTCAGATCCCTATGTCAAAAGTGAACCTGTACCATGCCAA 250
Qy 1155 aaagagaatctccaagaagaagactcatgtgaagaatgcaccccccaatgcagtttcaa 1214
Db 251 AAAGAGAATCTCTAAAGGAAGACACATGTGAAGAAATGCACGCCCAATGCAGTTCAA 310
Qy 1215 tgagctgttctgttgatattcttctgagcccttgaagataataagttgaatttt 1274
Db 311 TGAACCTCTTGTCTTGACATTCCTTGTGAGGCTCTAGAAAGAGATAGTGTGAATTTCT 370
Qy 1275 ggtttggattctgaagggggtcccgaaatgaggttaactcggcagctagctctgggtgc 1334
Db 371 GGTTTGGATTCGAAAGGGGATCCCGAAATGAGTGTGATGGCGGGTGTGCTCTGGGAGC 430
Qy 1335 agcagcagaaggaactggtggagagcactggaagaagatctgtgatacccccaggagaca 1394
Db 431 AGCAGCAGAGGAGCTGCTGGAGAGCAGCTGGAAGAGAGATCTGTGACTATCCACAGAGGCA 490
Qy 1395 aattgccaaagtgcagctgctctgtgaggttagcactcctagccg---tgagttggaact 1451
Db 491 AATCGCAAGTGGCAGCAGCTCTGTGATGTTAGCACCCCTTANCCGTGATGAATTGGAAC 550
Qy 1452 taaaggttttacta 1466
Db 551 TAACGATTTTACTA 565

RESULT 14
AW914163 712 bp mRNA EST 25-MAY-2000
LOCUS EST345467 Normalized rat brain, Bento Soares Rattus sp. cDNA clone
DEFINITION RGIAB26 5' end, mRNA sequence.
ACCESSION AW914163
VERSION AW914163.1 GI:8079837
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 712)
AUTHORS Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
Gene Index
JOURNAL Unpublished (1998)
COMMENT Other_ESTS: EST345466
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
This clone is available through the ATCC, contact the ATCC
Seq primer: M13 Reverse.
FEATURES
Source
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/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RGIAB26"
/clone_lib="Normalized rat brain, Bento Soares"
/notes="Organ: brain; Vector: p773Pac; Site_1: EcoRI;
Site_2: NotI"
BASE COUNT 185 a 145 c 178 g 204 t
ORIGIN

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